

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: markspencer

Timestamp: Mon Jul 30 10:42:47 EDT 2007

=====

Application No: 10588992 Version No: 2.0

Input Set:

Output Set:

Started: 2007-07-20 10:07:26.336

Finished: 2007-07-20 10:07:27.237

Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 901 ms

Total Warnings: 0

Total Errors: 0

No. of SeqIDs Defined: 16

Actual SeqID Count: 16

<110> SCHUIJFFEL, Danielle Francisca
NUIJTEN, Petrus Johannes Maria

<120> Ornithobacterium rhinotracheale subunit vaccines

<130> I-2004.011 US

<140> 10588992

<141> 2007-07-20

<150> 10/588992

<151> 2005-02-09

<150> PCT/EP2005/050577

<151> 2005-02-09

<150> EP 04075427.7

<151> 2004-02-11

<160> 16

<170> PatentIn version 3.3

<210> 1

<211> 1614

<212> DNA

<213> Ornithobacterium rhinotracheale

<220>

<221> CDS

<222> (1)..(1614)

<400> 1

```
atg gct gaa att ata aaa atg cca aga ttg agc gat acc atg gaa gaa      48
Met Ala Glu Ile Ile Lys Met Pro Arg Leu Ser Asp Thr Met Glu Glu
1              5              10              15
```

```
ggg aaa gtg gaa tct tgg aac aaa aaa gta gga gat aaa gta tca tac      96
Gly Lys Val Glu Ser Trp Asn Lys Lys Val Gly Asp Lys Val Ser Tyr
              20              25              30
```

```
ggc gac atc tta gcc gaa atc gaa aca gat aaa gcg gtt caa gaa ttt      144
Gly Asp Ile Leu Ala Glu Ile Glu Thr Asp Lys Ala Val Gln Glu Phe
              35              40              45
```

```
gaa aca gat gta gaa ggt act ctt tta tac atc ggt gta gag gct ggt      192
Glu Thr Asp Val Glu Gly Thr Leu Leu Tyr Ile Gly Val Glu Ala Gly
              50              55              60
```

```
caa gca gca cca gtt gat agt att tta gct atc atc ggt gca gaa ggc      240
Gln Ala Ala Pro Val Asp Ser Ile Leu Ala Ile Ile Gly Ala Glu Gly
65              70              75              80
```

```
gaa gac atc agc ggt ttg gta agc ggt gga ggt gct agc caa tca gcg      288
```

Glu Asp Ile Ser Gly Leu Val Ser Gly Gly Gly Ala Ser Gln Ser Ala	
85 90 95	
cca gct caa gaa gct gcc gct cct gca gaa gaa cca caa gcg gaa gct	336
Pro Ala Gln Glu Ala Ala Ala Pro Ala Glu Glu Pro Gln Ala Glu Ala	
100 105 110	
gca cca gcg gct gaa gtt cca gaa aat gta act atc gtt tct atg cca	384
Ala Pro Ala Ala Glu Val Pro Glu Asn Val Thr Ile Val Ser Met Pro	
115 120 125	
aga ttg agc gat acc atg gaa gaa ggt aaa gta gaa tct tgg aac aaa	432
Arg Leu Ser Asp Thr Met Glu Glu Gly Lys Val Glu Ser Trp Asn Lys	
130 135 140	
aaa gta gga gat aaa gta tca tac ggc gac atc tta gcc gaa atc gaa	480
Lys Val Gly Asp Lys Val Ser Tyr Gly Asp Ile Leu Ala Glu Ile Glu	
145 150 155 160	
aca gat aaa gcg gtt caa gaa ttt gaa aca gat gta gaa ggt act tta	528
Thr Asp Lys Ala Val Gln Glu Phe Glu Thr Asp Val Glu Gly Thr Leu	
165 170 175	
tta tat ata ggt gta gaa gct ggg caa tca gca cca gtt gat agc att	576
Leu Tyr Ile Gly Val Glu Ala Gly Gln Ser Ala Pro Val Asp Ser Ile	
180 185 190	
ttg gca atc atc gga cct gaa gga aca gat gtt tct gca atc gta gca	624
Leu Ala Ile Ile Gly Pro Glu Gly Thr Asp Val Ser Ala Ile Val Ala	
195 200 205	
gga ggt ggt gca aaa cca gct gct aaa gcg gaa gct cca aag gct gaa	672
Gly Gly Gly Ala Lys Pro Ala Ala Lys Ala Glu Ala Pro Lys Ala Glu	
210 215 220	
gca cct aag caa gct gct cca gca caa gag aaa aaa gaa act cca gcg	720
Ala Pro Lys Gln Ala Ala Pro Ala Gln Glu Lys Lys Glu Thr Pro Ala	
225 230 235 240	
cct gct gct cca aaa gca caa gct acc aac aat tca ggt aga gta ttt	768
Pro Ala Ala Pro Lys Ala Gln Ala Thr Asn Asn Ser Gly Arg Val Phe	
245 250 255	
att tct cca ttg gct aaa aaa ttg gct gat gaa aaa gga tac gat atc	816
Ile Ser Pro Leu Ala Lys Lys Leu Ala Asp Glu Lys Gly Tyr Asp Ile	
260 265 270	
aat caa att caa ggt aca gga gac aac gga aga atc atc aaa aaa gat	864
Asn Gln Ile Gln Gly Thr Gly Asp Asn Gly Arg Ile Ile Lys Lys Asp	
275 280 285	
gtt gaa aac ttt act cca caa gct gct gcg gct aag cca gct gtt gct	912
Val Glu Asn Phe Thr Pro Gln Ala Ala Ala Ala Lys Pro Ala Val Ala	
290 295 300	
ggg cca gtt gca ttg gaa gta gga gaa gat act gta atc cct aac tct	960
Gly Pro Val Ala Leu Glu Val Gly Glu Asp Thr Val Ile Pro Asn Ser	

305	310	315	320	
caa atg aga aaa gtg att gct aag cgt ctt tct gaa agt aaa ttt aca				1008
Gln Met Arg Lys Val Ile Ala Lys Arg Leu Ser Glu Ser Lys Phe Thr				
325		330	335	
gca cca cac tac tac tta acc att gaa gta gat atg gat aat gtg atg				1056
Ala Pro His Tyr Tyr Leu Thr Ile Glu Val Asp Met Asp Asn Val Met				
340		345	350	
gcg gct cgt aag caa atc aac caa att cca aat aca aaa gta tct ttc				1104
Ala Ala Arg Lys Gln Ile Asn Gln Ile Pro Asn Thr Lys Val Ser Phe				
355		360	365	
aac gat atc gta ttg aag gct act gct atg gct gtg aaa aaa cac cca				1152
Asn Asp Ile Val Leu Lys Ala Thr Ala Met Ala Val Lys Lys His Pro				
370		375	380	
gtg gta aat tca act tgg aaa gat aac gaa atc gta caa tac gct gct				1200
Val Val Asn Ser Thr Trp Lys Asp Asn Glu Ile Val Gln Tyr Ala Ala				
385		390	395	400
gta aac atc ggt gtt gca gtt gct gtt cca gat ggg ctt gta gta cct				1248
Val Asn Ile Gly Val Ala Val Ala Val Pro Asp Gly Leu Val Val Pro				
405		410	415	
gta gtg aaa aat aca gat tta aaa tca tta tct caa att tct gct gag				1296
Val Val Lys Asn Thr Asp Leu Lys Ser Leu Ser Gln Ile Ser Ala Glu				
420		425	430	
gta aaa gat tta gct aca aga tca aga gat aga aaa atc aaa gct gat				1344
Val Lys Asp Leu Ala Thr Arg Ser Arg Asp Arg Lys Ile Lys Ala Asp				
435		440	445	
gag atg gaa ggt tct acc ttt aca gtt tct aac cta gga gct tac ggt				1392
Glu Met Glu Gly Ser Thr Phe Thr Val Ser Asn Leu Gly Ala Tyr Gly				
450		455	460	
gta gaa agc ttt aca tca atc atc aat cag cca aac tct tgt atc ctt				1440
Val Glu Ser Phe Thr Ser Ile Ile Asn Gln Pro Asn Ser Cys Ile Leu				
465		470	475	480
tct gta ggt gcg att gta gaa aaa cca gtt gtt aaa aac gga caa atc				1488
Ser Val Gly Ala Ile Val Glu Lys Pro Val Val Lys Asn Gly Gln Ile				
485		490	495	
gta gtt ggt cac aca atg aaa ctt tgt tta gct tgc gat cac aga act				1536
Val Val Gly His Thr Met Lys Leu Cys Leu Ala Cys Asp His Arg Thr				
500		505	510	
gtg gac gga gca act gga agt act ttc cta caa act tta aaa caa tac				1584
Val Asp Gly Ala Thr Gly Ser Thr Phe Leu Gln Thr Leu Lys Gln Tyr				
515		520	525	
tta gag act cca atg tct atg ctt gtg tag				1614
Leu Glu Thr Pro Met Ser Met Leu Val				
530		535		

<210> 2
<211> 537
<212> PRT
<213> Ornithobacterium rhinotracheale

<400> 2

Met Ala Glu Ile Ile Lys Met Pro Arg Leu Ser Asp Thr Met Glu Glu
1 5 10 15

Gly Lys Val Glu Ser Trp Asn Lys Lys Val Gly Asp Lys Val Ser Tyr
20 25 30

Gly Asp Ile Leu Ala Glu Ile Glu Thr Asp Lys Ala Val Gln Glu Phe
35 40 45

Glu Thr Asp Val Glu Gly Thr Leu Leu Tyr Ile Gly Val Glu Ala Gly
50 55 60

Gln Ala Ala Pro Val Asp Ser Ile Leu Ala Ile Ile Gly Ala Glu Gly
65 70 75 80

Glu Asp Ile Ser Gly Leu Val Ser Gly Gly Gly Ala Ser Gln Ser Ala
85 90 95

Pro Ala Gln Glu Ala Ala Ala Pro Ala Glu Glu Pro Gln Ala Glu Ala
100 105 110

Ala Pro Ala Ala Glu Val Pro Glu Asn Val Thr Ile Val Ser Met Pro
115 120 125

Arg Leu Ser Asp Thr Met Glu Glu Gly Lys Val Glu Ser Trp Asn Lys
130 135 140

Lys Val Gly Asp Lys Val Ser Tyr Gly Asp Ile Leu Ala Glu Ile Glu
145 150 155 160

Thr Asp Lys Ala Val Gln Glu Phe Glu Thr Asp Val Glu Gly Thr Leu
165 170 175

Leu Tyr Ile Gly Val Glu Ala Gly Gln Ser Ala Pro Val Asp Ser Ile
180 185 190

Leu Ala Ile Ile Gly Pro Glu Gly Thr Asp Val Ser Ala Ile Val Ala
195 200 205

Gly Gly Gly Ala Lys Pro Ala Ala Lys Ala Glu Ala Pro Lys Ala Glu
210 215 220

Ala Pro Lys Gln Ala Ala Pro Ala Gln Glu Lys Lys Glu Thr Pro Ala
225 230 235 240

Pro Ala Ala Pro Lys Ala Gln Ala Thr Asn Asn Ser Gly Arg Val Phe
245 250 255

Ile Ser Pro Leu Ala Lys Lys Leu Ala Asp Glu Lys Gly Tyr Asp Ile
260 265 270

Asn Gln Ile Gln Gly Thr Gly Asp Asn Gly Arg Ile Ile Lys Lys Asp
275 280 285

Val Glu Asn Phe Thr Pro Gln Ala Ala Ala Ala Lys Pro Ala Val Ala
290 295 300

Gly Pro Val Ala Leu Glu Val Gly Glu Asp Thr Val Ile Pro Asn Ser
305 310 315 320

Gln Met Arg Lys Val Ile Ala Lys Arg Leu Ser Glu Ser Lys Phe Thr
325 330 335

Ala Pro His Tyr Tyr Leu Thr Ile Glu Val Asp Met Asp Asn Val Met
340 345 350

Ala Ala Arg Lys Gln Ile Asn Gln Ile Pro Asn Thr Lys Val Ser Phe
355 360 365

Asn Asp Ile Val Leu Lys Ala Thr Ala Met Ala Val Lys Lys His Pro
370 375 380

Val Val Asn Ser Thr Trp Lys Asp Asn Glu Ile Val Gln Tyr Ala Ala
385 390 395 400

Val Asn Ile Gly Val Ala Val Ala Val Pro Asp Gly Leu Val Val Pro
405 410 415

Val Val Lys Asn Thr Asp Leu Lys Ser Leu Ser Gln Ile Ser Ala Glu

420

425

430

Val Lys Asp Leu Ala Thr Arg Ser Arg Asp Arg Lys Ile Lys Ala Asp
 435 440 445

Glu Met Glu Gly Ser Thr Phe Thr Val Ser Asn Leu Gly Ala Tyr Gly
 450 455 460

Val Glu Ser Phe Thr Ser Ile Ile Asn Gln Pro Asn Ser Cys Ile Leu
 465 470 475 480

Ser Val Gly Ala Ile Val Glu Lys Pro Val Val Lys Asn Gly Gln Ile
 485 490 495

Val Val Gly His Thr Met Lys Leu Cys Leu Ala Cys Asp His Arg Thr
 500 505 510

Val Asp Gly Ala Thr Gly Ser Thr Phe Leu Gln Thr Leu Lys Gln Tyr
 515 520 525

Leu Glu Thr Pro Met Ser Met Leu Val
 530 535

<210> 3
 <211> 1572
 <212> DNA
 <213> Ornithobacterium rhinotracheale

<220>
 <221> CDS
 <222> (1)..(1572)

<400> 3
 atg aaa ata aat tac aaa aat ata ctt tta agt gct agc gtt ctc ttt 48
 Met Lys Ile Asn Tyr Lys Asn Ile Leu Leu Ser Ala Ser Val Leu Phe
 1 5 10 15
 ttt gca gca tgt agc gat ttt gat tac aat gta gaa aac cca aac ctc 96
 Phe Ala Ala Cys Ser Asp Phe Asp Tyr Asn Val Glu Asn Pro Asn Leu
 20 25 30
 acg aag gga gag gct gat ttc tct aaa tat gta gct tta gga aat tct 144
 Thr Lys Gly Glu Ala Asp Phe Ser Lys Tyr Val Ala Leu Gly Asn Ser
 35 40 45
 ctc act tct ggt tat tca gac gga gcc tta tat cgc tcg gca caa gag 192
 Leu Thr Ser Gly Tyr Ser Asp Gly Ala Leu Tyr Arg Ser Ala Gln Glu
 50 55 60

aat	tca	tac	ccc	gca	atc	att	gcc	aaa	caa	atg	aaa	tat	gta	ggc	ggg	240
Asn	Ser	Tyr	Pro	Ala	Ile	Ile	Ala	Lys	Gln	Met	Lys	Tyr	Val	Gly	Gly	
65					70					75					80	
ggc	gag	ttc	tct	caa	cct	ttg	atg	aaa	gac	aac	att	ggg	ggg	ttt	tcg	288
Gly	Glu	Phe	Ser	Gln	Pro	Leu	Met	Lys	Asp	Asn	Ile	Gly	Gly	Phe	Ser	
				85					90					95		
gat	ttg	ttt	gaa	gca	agt	aaa	cac	acc	gca	ttt	tac	gga	aaa	tta	gaa	336
Asp	Leu	Phe	Glu	Ala	Ser	Lys	His	Thr	Ala	Phe	Tyr	Gly	Lys	Leu	Glu	
			100					105					110			
tta	aaa	atc	gta	gac	ggg	gca	cct	acg	cca	gtg	cct	tct	gtg	cct	aag	384
Leu	Lys	Ile	Val	Asp	Gly	Ala	Pro	Thr	Pro	Val	Pro	Ser	Val	Pro	Lys	
		115					120					125				
ttt	agt	tta	gct	caa	acc	ttc	gta	aaa	ggg	aat	ttt	aat	aat	ttg	ggc	432
Phe	Ser	Leu	Ala	Gln	Thr	Phe	Val	Lys	Gly	Asn	Phe	Asn	Asn	Leu	Gly	
	130					135					140					
gtg	cca	ggg	gct	aaa	tct	tat	cat	tta	tta	gct	caa	ggg	tac	gga	aat	480
Val	Pro	Gly	Ala	Lys	Ser	Tyr	His	Leu	Leu	Ala	Gln	Gly	Tyr	Gly	Asn	
145					150					155					160	
att	gct	aat	ctg	aag	gag	agt	aaa	gcc	aat	cca	tat	ttt	gtg	cga	ttt	528
Ile	Ala	Asn	Leu	Lys	Glu	Ser	Lys	Ala	Asn	Pro	Tyr	Phe	Val	Arg	Phe	
			165					170					175			
gct	agc	caa	cca	aat	gcc	agc	gtg	ctg	agc	gat	gct	ttg	gca	caa	aaa	576
Ala	Ser	Gln	Pro	Asn	Ala	Ser	Val	Leu	Ser	Asp	Ala	Leu	Ala	Gln	Lys	
			180					185					190			
cct	aca	ttc	ttt	acc	tta	tgg	atc	ggg	aac	aac	gat	gtt	tta	ggc	tat	624
Pro	Thr	Phe	Phe	Thr	Leu	Trp	Ile	Gly	Asn	Asn	Asp	Val	Leu	Gly	Tyr	
		195					200					205				
gcc	atg	aat	ggc	gca	gca	agc	aca	gat	cga	aaa	ggg	aac	cct	gat	gta	672
Ala	Met	Asn	Gly	Ala	Ala	Ser	Thr	Asp	Arg	Lys	Gly	Asn	Pro	Asp	Val	
	210					215					220					
aca	aca	tat	aat	tca	aat	gat	ttg	tct	gat	gct	aac	ttg	gtg	gca	ggc	720
Thr	Thr	Tyr	Asn	Ser	Asn	Asp	Leu	Ser	Asp	Ala	Asn	Leu	Val	Ala	Gly	
225					230					235					240	
tct	att	caa	aaa	tta	gta	aaa	gca	ctt	aca	gat	tca	ggc	gca	aaa	ggg	768
Ser	Ile	Gln	Lys	Leu	Val	Lys	Ala	Leu	Thr	Asp	Ser	Gly	Ala	Lys	Gly	
			245					250					255			
gct	gta	gcg	aat	ttg	cct	tat	gtc	gaa	gac	att	ccg	tat	ttt	aca	acc	816
Ala	Val	Ala	Asn	Leu	Pro	Tyr	Val	Glu	Asp	Ile	Pro	Tyr	Phe	Thr	Thr	
			260					265					270			
gtg	ccg	gct	gag	cct	tta	agc	cct	tta	aac	aaa	agt					

att gaa aat ttg aat aaa ttt tat gct agc cta aat aaa gtt ttt gat	912
Ile Glu Asn Leu Asn Lys Phe Tyr Ala Ser Leu Asn Lys Val Phe Asp	
290 295 300	
gcc cta gga gca agc gat aga aaa atc aca ttt aat gcc gat aaa gca	960
Ala Leu Gly Ala Ser Asp Arg Lys Ile Thr Phe Asn Ala Asp Lys Ala	
305 310 315 320	
agc ggt gct gtg att gta gat aaa agt ttg cca gat tta agt caa aaa	1008
Ser Gly Ala Val Ile Val Asp Lys Ser Leu Pro Asp Leu Ser Gln Lys	
325 330 335	
atc tta gca acc tta cta aaa tta gaa ttc cca aac gaa aaa gct aaa	1056
Ile Leu Ala Thr Leu Leu Lys Leu Glu Phe Pro Asn Glu Lys Ala Lys	
340	